

FIG. 1

1 CCCTTCTCCAGGACTCTGGCTGCCAGAGCTCCGCCTTTCAGATCAATTCTCGACCAC 60
 61 CACCTTGGGACTGCGGCCAGTCTGCCCTCTGGATCAGTGGGTCCAGACACGCCCCCT 120
 121 CCAGGACCTCAAAGCACCCCGACCTAAGTCACCGCCCACTGGCCCCAGACGCACTGG 180
 181 GCTCCGCTGACTCTCTTGACACCTCTGGGAGGAATGCTCCCTGTCTGCCATCGTTT 240
 M L P V C H R F
 241 TTGCGACCACTCCTCCTCTCTGTCTTGTGCGCTCGACGACCTGGCCCCCGCCGACG 300
 C D H L L L L L L L P S T T L A P A
 301 ATCCATGGGCCCCGCTGCCGCTGCTCCAGTTCTTGGCTTCCCGAAGCGCCCCGGAG 360
 S M G P A A A L L Q V L G L P E A P R S
 361 CGTCCCAACACCGACTGTGCTCTCTGTCTGTGCGGCTATTCCGTGCGCTGACCC 420
 V P T H R P P V P P V M W R L F R R D P
 421 CCAGGAGCCAGAGTGGACGCGCTCTGCGGCCATGCCACGTGGAGGAAGTAGGGTGCG 480
 Q E A R V G R P L R P C H V E L G V A
 481 CGGAACATGTGCGCCACATCCCGACAGCGTCTGTCTCCAGGCCCGCACACCCGC 540
 G N I V R H I P D S G L S S R P A Q P A
 541 CAGGACCTCGGGGTGTGCCCCGAGTGGACAGTCGTCTTTCACCTGTGCAATGTGGAGCC 600
 R T S G L C P E W T V V F D L S N V E P
 601 CACAGAGCGCCCAACACGCGCGCTTAGAGTTGCGGCTGGAGGCTCAGTGTGAAGATAC 660
 T E R P T R A R L E L R L E A E C E D T

FIG. 2a

661 AGAGGTGGAGCTAAGCTGGCACTGTGGCGGCACGACAGCATCCAGGCGCTGAGCT 720
 G G W E L S V A L W A D A E H P G P E L
 721 GCTCGGGTGGCGGCACACAGGGGTGCTCTCGCGGCAGACCTACTGGGGACTGCACT 780
 L R V P A P P G V L L R A D L L G T A V
 781 AGCGCCAAACCATCAGTCCCTGTACTGTGGCGCTGGCGCTGTCACTGCACCCCTGGGGC 840
 A A N A S V P C T V R L A L S L H P G A
 841 CACTGACCTGTGGCGCCTGGCTGAGGCGCTCCCTGCTGTGTGACGCTGGACCCACG 900
 T A A C G R L A E A S L L L V T L D P R
 901 CCTGTCTCCCTGGCGGCATTGGCGGCACACGAGCCAGGCTAGAAGTTGGTCCAGT 960
 L C P L P R L R R H T E P R V E V G P V
 961 GGGCACTTGTCTACCCGACGTTGCATGTGAGCTTCGCTGAGGTGGCTGGCACCCTTG 1020
 G T C R T R R L H V S F R E V G W H R W
 1021 GGTGATCGCGCGCTGGCTTCTAGCCAACTTCTGCCAGGCACGTGGCACTACCCGA 1080
 V I A P R G F L A N F C Q G T C A L P E
 1081 AACGTGAGGGACCGCGCGCGCTGCACCTCAACACGCTGTGCTGCGCGCGCTCAT 1140
 T L R G P G P P A L N H A V L R A L M
 1141 GCACGAGTGTCCCAACCGGGTGCAGGCTCGCCCTGCTGCCAGAGCGTCTATC 1200
 H A A A P T P G A G S P C C V P E R L S
 1201 ACCCATCTCGTCTCTCTTCGACAATAGTGACAACGTGGTCTCGGACACTACGAAGA 1260
 P I S V L F F D N S D N V V L R H Y E D
 1261 CATGTGTGTGATGAGTGTGGCTGGCGTTGACCAACCGGGACACCCCTTCAGGACCGCC 1320
 M V V D E C G C R
 1321 CCACGCAAGCAGGAGCTGTTGTTCATGTTTTATTGTGTACAAAAGCTTAAACAAA 1380
 1381 TTGACT 1387

FIG. 2b

GDF-1 RRHTEFVEVG--PVGTCTRRRLHVSF-REVGNHRWVIAPRGFLANFQGTALPETLRGPGGPP
 Vg-1 KRKSYKLPFT--ASNIKKRHLYVEF-KDVGNQNWVIAPOGYMANVYGECP-YPLTEILNG--
 Vgr-1 CSGSDYNGSE--LKTAKKHLYVSF-QDLGWQDWIIVAPAGYAAVYEDGEC-SFPLNAHNA--
 BMP-2a KRQAKKQQRK--LKSSKKRHLYVDF-SDVGWNDWIVAPPGYHAFYEDGEC-SFPLADHNS--
 BMP-2b SPKHHQQRK--KKNKRRHSLYVDF-SDVGWNDWIVAPPGYQAFYEDGEC-SFPLADHNS--
 BMP-3 TLKKARKQWI--EPRNKKRRLKVDL-ADIGWSEWISPSFSDAYVYSGGAFQFMPKSLKPS--
 DPP -HARRPTRKN--HDDTKRRHSLYVDF-SDVGWDDWIVAPGLYDAYVYHIGKCP-FPLADHENS--
 MIS GRAORSACATA--ADGPAALRELSDVLRAE-PSVLIPETYOQANNVYGGVGPQSDRNPY--
 inhibin α RLLORPEEPA--AHANCHRVALNISF-QELGWRWIVPSPFVFHYVGGGLHPPNLSLPV-
 inhibin β GLE--CDGKV--NIC-KKQEFFVSF-KDIGWNDWIIAPSGYHANYEDGECPSHIAGTSGSSL-
 inhibin β GLE--CDGRT--NIC-KKQEFFVSF-KDIGWNDWIIAPSGYHANYEDGECPSHIAGTSGSSL-
 inhibin β ALDTNYCESST--EKNCVROLYIDFRKDLGK-WIHEPKGYHANFAGGCP-YLW----SAD-
 TGF- β 1 ALDAAACERNV--QNCCLRLRLYIDFRKDLGK-WIHEPKGYANFAGGCP-YLW----SAD-
 TGF- β 2 ALDAAACERNV--QNCCLRLRLYIDFRKDLGK-WIHEPKGYANFAGGCP-YLW----SAD-
 TGF- β 3 ALDAAACERNV--QNCCLRLRLYIDFRKDLGK-WIHEPKGYANFAGGCP-YLW----SAD-
 TGF- β 4 ALDAAACERNV--QNCCLRLRLYIDFRKDLGK-WIHEPKGYANFAGGCP-YLW----SAD-
 TGF- β 5 GVGQEQYCEGNN--GPNCQVKP-LYINFRKDLGK-WIHEPKGYEANYCLGNCP-YLW----SMD-

FIG. 3a

	GDF-1	Vg-1	Vgr-1	BMP-2a	BMP-2b	BMP-3	DPP	MIS	Inhibin α	Inhibin βA	Inhibin βB	TGF- $\beta 1$	TGF- $\beta 2$	TGF- $\beta 3$	TGF- $\beta 4$	TGF- $\beta 5$
GDF-1	100	52	40	38	39	41	34	33	22	31	31	26	27	30	26	26
Vg-1	-	100	59	59	57	45	49	27	23	45	40	34	35	38	33	35
Vgr-1	-	-	100	62	59	43	57	26	23	45	39	35	37	38	37	37
BMP-2a	-	-	-	100	92	44	73	26	20	42	37	34	34	35	33	33
BMP-2b	-	-	-	-	100	44	74	27	21	41	37	33	34	35	33	33
BMP-3	-	-	-	-	-	100	42	25	28	33	33	29	31	31	26	28
DPP	-	-	-	-	-	-	100	25	20	39	36	35	35	35	35	34
MIS	-	-	-	-	-	-	-	100	18	22	22	24	21	26	25	24
Inhibin α	-	-	-	-	-	-	-	-	100	23	21	24	23	24	24	24
Inhibin βA	-	-	-	-	-	-	-	-	-	100	63	38	37	36	35	38
Inhibin βB	-	-	-	-	-	-	-	-	-	-	100	35	35	36	34	32
TGF- $\beta 1$	-	-	-	-	-	-	-	-	-	-	-	100	73	77	85	81
TGF- $\beta 2$	-	-	-	-	-	-	-	-	-	-	-	-	100	81	68	69
TGF- $\beta 3$	-	-	-	-	-	-	-	-	-	-	-	-	-	100	74	73
TGF- $\beta 4$	-	-	-	-	-	-	-	-	-	-	-	-	-	-	100	78
TGF- $\beta 5$	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	100

FIG. 3b

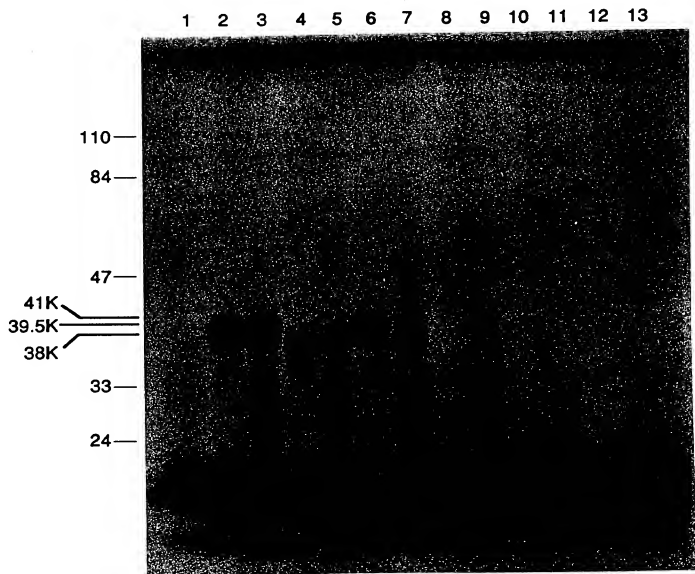


FIG. 4

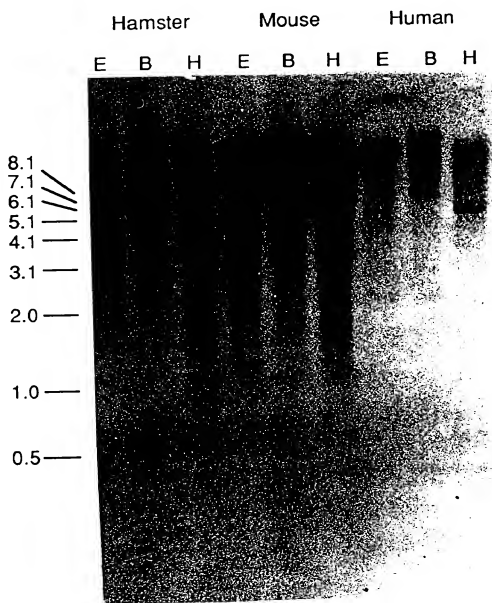


FIG. 5

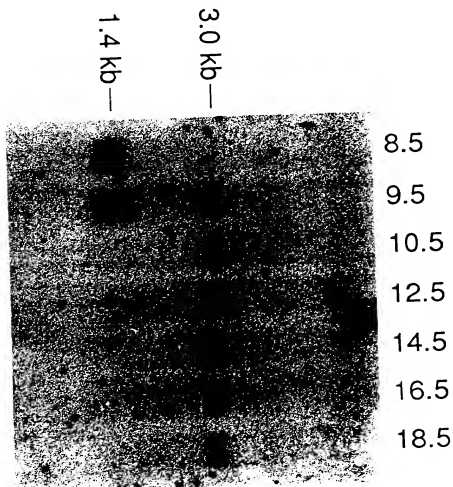



FIG. 6

3.0 kb -



10.5 d placenta
testis
seminal vesicle
ovary
oviduct
uterus
brain
thymus
heart
lung
kidney
adrenal
spleen
liver
intestine
pancreas

FIG. 7

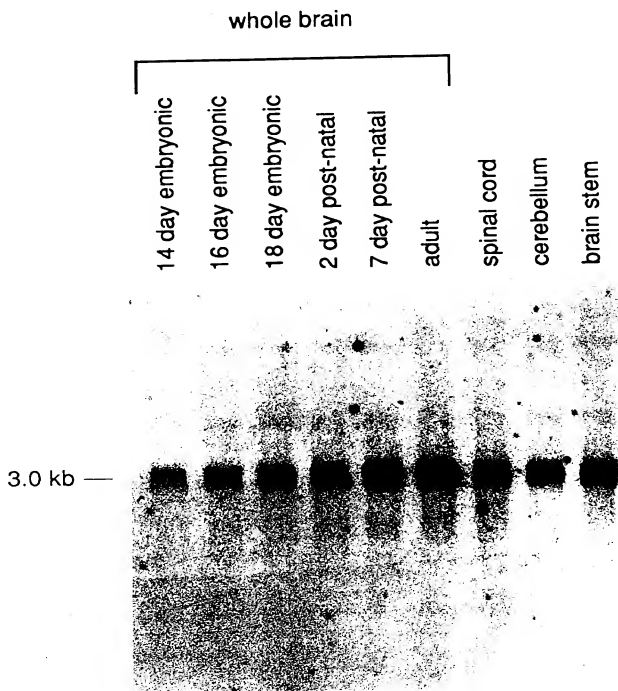


FIG. 8

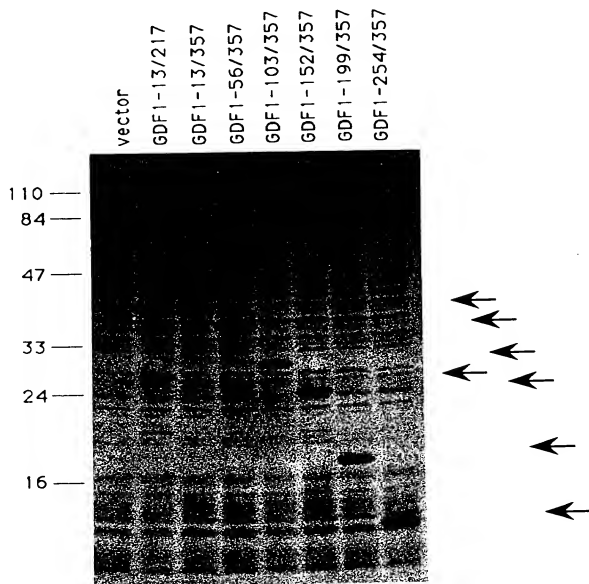


FIG. 9

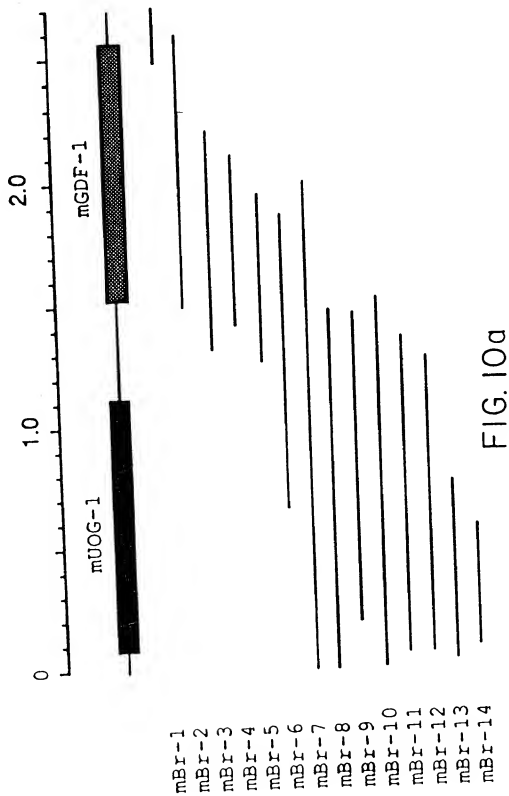


FIG. 10a

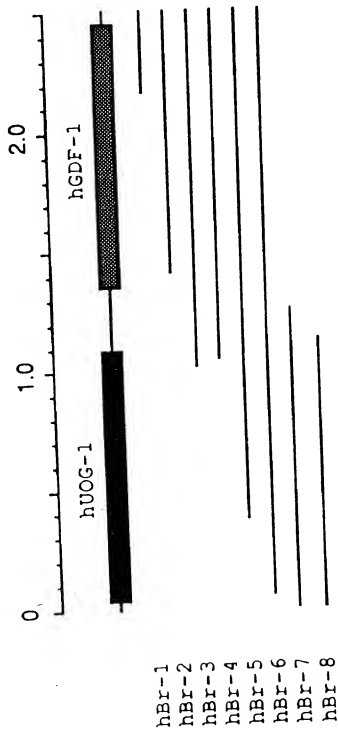


FIG. 10b

1 GCGCGTGACGCGGAGGGCGCGGCGACTCGGACCGGTGACGGCAACAGCGGAGACAGCGG 60
 61 AGAATTGGATAGCATGGCTGCTGCCGCGGCGACCCCAAGGCTCGAGGGCGCCAGGCCAT 120
 M A A A A A T P R L E A P E P H
 121 GCGCAGTTATGCGCAGATGTTGCAACGAAGCTGGCGCTCGGCCCTGGCGGGCGGCTCAGGG 180
 P S Y A Q M L Q R S W A S A L A A A Q G
 181 CTGGCGGGAGCTGCGGCTGGGACTGGCGCGCGCGGCTGGCGGAGCACGCGGCACCTGGC 240
 C G D C G W G L A R R G L A E H A H L A
 241 TGCACCCGAGCTGCTGCTGGCCGTGCTCTGCGCTCTGGGGTGGACAGCGTTCGCGCTGGC 300
 A P E L L L L A V L C A L G W T A L R W A
 301 AGCCACACACACATCTTTTGGGCCCCGGCCAAAGCGGTGTCGTCTGCAGCCTAGAGATGC 360
 A T T H I F R P L A K R C R L Q P R D A
 361 TGCCAGGTTACCTGAGAGCGCCTGGAAGCTTCTGTTCTACTTGGCCTGTTGGAGTACTG 420
 A R L P E S A W K L L F Y L A C W S Y C
 421 CGCTTACCTGCTCCTGGGCACCAAGTTATCTTCTTCCATGACCCCGCCTCTGCTTCTA 480
 A Y L L L L G T S Y P F F H D P P S V F Y
 481 TGACTGGAGGTGACGGCATGGCAGTGCCTGGGACATCGCGGTGGCCTATTGCTGACGG 540
 D W R S G M A V P W D I A V A Y L L Q G
 541 GAGTTTCTACTGCGCACTCCATCTATGCCACCGTGTACATGGACAGCTGGCGTAAGGACTC 600
 S F Y C H S I Y A T V Y M D S W R K L S
 601 GGTGGTCTGCTGGTGATCAGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
 V V M L V H H V V T L L L I A S S Y F A
 661 CCGGTACCCACAACGTAGGCGCTCCTCGTGTCTTCTGTCATGACGTGACGGATGTCAGCT 720
 R Y H N V G L L V F F L H D V S D V Q L
 721 GGAGTTCACAAAACCTCAACATCTACTTTAAGGCTAGGGGTGGTGCCTACCATCGCTTGA 780
 E F T K L N I Y F K A R G G A Y H R L H
 781 TGGGCTGGTGCCCAACCTGGGCTGCTCAGCTTCTGTTTCTGCTGGTCTGGTTCGGCCT 840
 G L V A N L G C L S F C F C W F W F R L
 841 CTACTGGTTCGGCTCAAGGTTCTGTACGCCACTTGCCACTGCAGCCTGCAGTCTGTGCC 900
 Y W F P L K V L Y A T C H C S L Q S V P
 901 TGACATTCCGTACTACTTCTTCTTCAACATTCTGCTGTGCTGCTGATGGTCATGAACAT 960
 D I P Y Y F F F F N I L L L L L M V M N I
 961 CTATTGGTTCCTGTACATTGTTGGCTTTCGACGCCAAGGTGCTGACTGGTCAGATGGGTGA 1020
 Y W F L Y I V A F A A K V L T G Q M R E
 1021 ACTGGAAGACTTGAGGGAGTACGACACTCTGGAAGCTCAGACAGCCAGCCCTGCAAAAGC 1080
 L E D L R E Y D T L E A Q T A K P C K A
 1081 CGAGAAGCCACTGAGGAATGGCTGGTGAAGGACAAGCTCTTCTGAGTCTCTTGTGCTCA 1140
 E K P L R N G L V K D K L F
 1141 ACTTCAGCCATCCAGGACTCTATCCCATCTACCTGGGATACTGACTCCGCCCTGGAGA 1200
 1201 CTCGACCCAGTCCCTGGAGGTCTGCTCCACCCCTGGAGGCCGCTCCCGCTTTGGCGG 1260
 1261 CATTGGCCTCGCCCTAGGACAATAGCCCGCCCTAAGATTAGGATGCTACCTTCTCCA 1320
 1321 GGGACTCTGGCTGCCAGCAGCTCCGCCCTTCAGATCAATTCTCGACACCCACCTTGGGA 1380
 1381 CTGCGGCCAGTCTGCTGCTGATCAGTGGGTCCAGACACGCCGCCCTCCAGGACCTC 1440
 1441 AAAGCACCCCGACCTAAGGTACCCAGCCCACTGGCCCCAGACAGCAGTGGGCTCCGCTGA 1500
 1501 CTCTCTGGACACCTCTCGGGAGGAAAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1560
 M L P V C H R F C D H

FIG. 11a

1561 CTCCTCCTCCTGCTCTTGCTGCCCTCGACGACCTGGCCCCGCCAGCATCCATGGGC 1620
 L L L L L B L P S T T L A P A P A S H G
 1621 CCCGCTGCCCGCTCCTCCAGGTTCTTGGGCTTCCCGAAGCGCCGAGCGTCCCCACA 1680
 P A A A L L Q V L G L P E A P R S V P T
 1681 CACCGACCTGTGCCTCCTGTCTATGTGGCGCCTATTCCGTGCCCGGACCCCGAGGAGGCC 1740
 H R P V P P V M W R L F R R R R D P Q E A
 1741 AGAGTGGGAGCGCCTCTCGGGCCATGCCAGTGGAGGAATAGGGGTGCGCGGAAACATT 1800
 R V G R P L R P C H V E E L G V A G N I
 1801 GTGGCCACATCCCGACAGCGGTCTGTCTCCAGGCCCGCACAAACCGCCAGGACCTCG 1860
 V R H I P D S G L S S R P A Q P A R T S
 1861 GGGCTGTGCCCGAGTGGACAGTCGTCTTTGACCTGTGGAATGTGGAGCCACAGAGCGC 1920
 G L C P E W T V V F D L S N V E P T E R
 1921 CCAACACGCGCGCCTTAGAGTTGCGGCTGGAGGCTGAGAGTGAAGATACAGGGGGGTGG 1980
 E L S V A L W A D A E H P G P E L L R V
 1981 GAGCTAAGCGTGGCACTGTGGCGGACGACAGCATCCAGGGCCTGAGCTGTGCGCGTG 2040
 F T R A R L E L R L E A E S E D T G G W
 2041 CCGCGCCACACAGGGGTCTCCTGCGCGCAGACCTACTGGGGACTGCAGTAGCGGCCAAC 2100
 P A P P G V L L R A D L L G T A V A A N
 2101 GCATCAGTGCCTGTACTGTGCGCCTGGCGCTGTCACTGCACCTGGGGCCACTGCAGCC 2160
 A S V P C T V R L A L S L H P G A T A A
 2161 TGTGGGCGCTGGCTGAGGCCCTCCCTGCTGCTGGTGACGCTGGACCCACGCTGTGTCCC 2220
 C G R L A E A S L L L V T L D P R L C P
 2221 TTGCGCGATTGCGCGGCCACAGGAGCCCGAGGTAGAAGTTGGTCCAGTGGGCACTTGT 2280
 L P R L R R H T E P R V E V G P V G T C
 2281 CGTACCCGACGGTGCATGTGAGCTTCCGTGAGGTGGGCTGGCACCGTTGGGTGATCGCG 2340
 R T R L H V S F R E V G W H R W V I A
 2341 CCGCGTGGCTTCTAGCCAACCTTGCAGGGCAGCTGCGCACTACCCGAAACGCTGAGG 2400
 P R G F L A N F C Q G T C A L P E T L R
 2401 GGACCCGCGCGCGCCTGCACTCAACACGCTGTGCTGCGCGCGCTCATGCACGCGAGT 2460
 G P G P P A L N H A V L R A L M H A A
 2461 GCTCCACCCCGGGTGACGGCTCGCCCTGCTGCGTGCCAGAGCGTCTATCACCCTCTCC 2520
 A P T P G A G S P C C V P E R L S P I S
 2521 GTGCTCTTCTTCGACAATAGTGACAACGTGGTCCCTGCGACACTACGAAGACATGGTGGT 2580
 V L F F D N S D N V V L R H Y E D M V V
 2581 GATGAGTGTGGCTGCCGTGTGACCAACCGGGACACCCCTTTCAGGGACCGCCCCACGCAAAA 2640
 D E C G C R
 2641 GCAGGGACTGTTTGTTCATGTTTATTGGTGACAAAAAGCTTAAAAAAATTTGACTAAA 2700
 2701 AATTAAGTTCC 2711

FIG. 11a CONT.'

1 GGACACGGCGGGCGAGCGGGCGGTATGCGCGGGCGGGGCGCGCGGGGCCGACGGGG 60
 P E P M P S Y A Q L V Q R G W G S A L A 120
 61 CCCGAGCCCCATGCCGAGCTACGCCAGCTAGTGCAGCGCGGCTGGGGCAGCGCGCTGGCG 120
 GCGGCGCGGGGCTGCACGGACTGCGGGCTGGGGGCTGGCGCGTCCGGGCTGGCTGAGCAC 180
 121 A A R G C T D C G W G L A R R G L A E H 180
 GCGCACCTGGCGCGCGGAGCTGCTGCTGCTGGCGCTCGGGCGCGCTGGGCTGGACCGG 240
 181 A H L A P P E L L L L L A L G A L G W T A 240
 CTGCGCTCCGGCGCCACTGCGCGCTCTTTGCGCCCTGGCGAAGCGGTGCTGCCTCCAG 300
 241 L R S A A T A R L F R P L A K R C C L Q 300
 CCCAGAGATGCCGCCAAGATGCCGAGAGCGCTTGGAACTTTCTTCTACCTGGGCAGC 360
 301 P R D A A K M P E S A W K F L F Y L G S 360
 TGGAGCTACAGTGCTTACCTGCTGTTTGGCACCAGCTACCCCTTCTTCCATGACCACCA 420
 361 W S Y S A Y L L F G T D Y P F F H D P P 420
 421 TCTGCTTCTACGACTGGACGCCGGCATGGCACTGCCACGGGACATTGCAGCGCGCTAC 480
 S V F Y D W T P G M A V P R D I A A A Y 480
 481 CTGCTCCAGGGAAGCTTCTATGGCCACTCCATCTACGCTACGCTATACATGGACACCTGG 540
 L L Q G S F Y G H S I Y A T L Y M D T W 540
 541 CGCAAGGACTCGGTGGTCTGCTGCTCCACCACTGGTCACTCTCATCTCTAGTCTCC 600
 R K D S V V M L L H H V V T L I L I V S 600
 601 TCCTACGCGCTTCCGGTACCACAATGCGGCATCTTGTGCTCTTCTGACGATATCAGT 660
 S Y A F C R Y H N V G I L V L F L H D I S 660
 661 GACGTGCAGCTTGAGTTACCAAGCTCAACATTTACTTCAAGTCCCGCGGCGCTCCTAC 720
 D V Q L E F T K L N I Y F K S R G G S Y 720
 721 CATCGGCTGCATCTTGGCAGCAGACTTGGGCTGCCTCAGCTTCGGGCTTCACTGGTTC 780
 H R L H A L A A D L G C L S F G F S W F 780
 781 TGGTTCCGCTCTACTGGTTCCCGCTCAAGTCTGTATGCCACCACTGCTGACGCTG 840
 W F R L Y W F P L K V L Y A T S H C S L 840
 841 CGCAGCTGCTGACATCCCTTCTACTTCTTCTTCAATGCGCTCTGCTGCTGCTCACC 900
 R T V P D I P F Y F F F N A L L L L T 900
 901 CTTATGAACCTCTACTGGTTCTGTATCATCGTGGCGTTTGACAGCAAGGTGTTGACAGC 960
 L M N L L Y W F L Y I V A F A A K V L T G 960
 961 CAGGTGCACAGCTGAAGACCTGCGGGAGTATGACACGCGGAGGCGCCAGAGCCTGAAG 1020
 Q V H E L K D L R E Y D T A E A Q S L K 1020
 1021 CCCAGCAAGCGGAGAAGCCACTGAGGAACGGCTGGTGAAGGACAAGCGCTTCTGAACC 1080
 P S K A E K P L R N G L V K D K R F 1080
 1081 CCTCGGCGCGCGCGCGGACCGCGGCGCCCGGAAATCCCGCGCCAGGCTCCCCGTC 1140
 1141 CTTGGCGCGCGCTCCACCGCTTCAACTCTGCTCTTACGGCGCGCGCCACCTCCCTG 1200
 1201 GGACCCCGCGCGCTCATCTGCTTCACTTCCCGCGCCCGCGCGGACCGCTGCGCC 1260
 1261 TCCGGGGACACCGCGCGCGCTCAGCCACTGCTCCCGGCGCGCGCGGACCGCTGCGCA 1320
 1321 CTCTCTGCTATCGCTGGGAGGAAGATGCCACCGCGCGGCAAGGTCCCTCGGGCCACC 1380
 H P P P Q Q G P C G H H

FIG. 11b

1381 ACCTCCTCCTCCTCCTGGCCCTGCTGCTGCCCTGCTG⁻CCCTGACCCGGGCCCCCGTGC 1440
 L L L L L L L A L L L L P S L P L T R A P V P
 1441 CCCCAGGCCAGCCGCGCCCTGCTCCAGGCTCTAGGACTGGCGATAGGCCCCAGGGTG 1500
 P G P A A A L L Q A L G L R D E P Q G A
 1501 CCCCCAGGCTCCGCGCGGTTCCCCCGGTTCATGTGGCGCTGTTTCGACGCGGGGACCCCC 1560
 P R L R P V P P V M W R L F R R R D P Q
 1561 AGGAGACCAAGTCTGGCTCGCGCGGACGTCCCAGGGGTCAACCCTGCAACCGTGCCACG 1620
 E T R S G S R R T S P G V T L Q P C H V
 1621 TGGAGGAGCTGGGGGTGCGCGGAAACATCGTCCGCCACATCCCGAGCCGCGGTGCGCCCA 1680
 E E L G V A G N I V R H I P D R G A P T
 1681 CCGGGGCTCGGAGCCTGTCTCGGCGCGGGCAITGCCCTGAGTGGACAGTCGTCTTCG 1740
 R A S E P V S A A G H C P E W T V V F D
 1741 ACCTGTCCGCTGTGGAACCCGCTGAGCGCCCGAGCCGGGCGCGCTGGAGCTGCGTTTCG 1800
 L S A V E P A E R P S R A R L E L R F A
 1801 CCGCGCGCGCGCGGAGCCCGGAGGGCGCGCTGGGAGCTGAGCGTGGCGCAAGCGGGCC 1860
 A A A A A A P E G G W E L S V A Q A G Q
 1861 AGGGCGCGGGCGCGGACCCCGGGCGCGTGTCTCGCCAGTTGGTCCCGCCCTGGGGC 1920
 G A G A D P G P V L L R Q L V P A L G P
 1921 CGCCAGTGGCGCGGAGCTGCTGGGCGCGCTTGGGCTCGCAACGCCTCATGGCCGCGCA 1980
 P V R A E L L G A A W A R N A S W P R S
 1981 GCTTCGCGCTGGCGCTGGCGCTACGCCCCCGGGCCCTGCGCGTGGCGCGCGCTGGCGG 2040
 L R L A L A L R P R A P A A C A R L A E
 2041 AGGCCTCGCTGCTGCTGGTGAACCTCGACCCGCGCTGTGCCACCCCTGGCCCGGGCGC 2100
 A S L L L V T L D P R L C H P L A R P R
 2101 GCGCGACGCCGAACCCGTGTTGGGCGCGCGCCCGGGGGCGCTGTGCGCGCGCGCGGC 2160
 R D A E P V L G G P G G A C R A R R L
 2161 TGTACGTGAGCTTCGCGGAGTGGGCTGGCACCCTGGGTATCGCGCGCGCGCTTCC 2220
 Y V S F R E V G W H R W V I A P R G F L
 2221 TGGCCAACTACTGCCAGGCTCAGTGGCGCTGCCCGCTCGCGCTGTGGGGTCCGGGGGG 2280
 A N Y C Q G Q C A L P V A L S G S G G P
 2281 CGCGGGCGCTCAACCAAGCTGTGCTGCGCGCTCATGCACGCGCGCGCGCGGAGCCG 2340
 P A L N H A V L R A L M H A A P G A A
 2341 CGACCTGCGCTGCTGCGTGC CGCGCGCTGTGCGCCATCTCCGTGCTCTTCTTTGACA 2400
 D L P C V P A R L S P I S V L F F D N
 2401 ACAGCGACACCTGGTGTGCGCGGAGTATGAGGACATGGTGGTGGACAGTGGCGGCTGCC 2460
 S D N V V L R Q Y E D M V V D E C G C R
 2461 GCTAACCCGGGGCGGGCAGGAGCGGGGCCAACAAATAATGCCGCGTGG 2510

FIG. 11b CONT.'

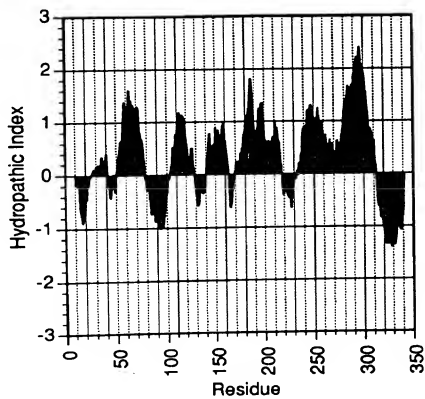


FIG. 12

167 225
 mGDF-1 ELLRVPAPP-GVLLRADLLGTAAANASVPTVRLALSLHPGATAACGRLAESLLLVTL
 181 240
 hGDF-1 VLLRQLVPALGPPVRAELLGAAWARNASWPRSLRLALALRPAPACARLAESLLLVTL
 226 284
 mGDF-1 DPRLC-PLPRIRRHTEPRVEVGPVGTTRRLHVSFREVGVHWRWVIAPRGFLANFQGGTQ
 241 300
 hGDF-1 DPRLCHPLARPRDAEPVLGGPGGAGARRLLYVSFREVGVHWRWVIAPRGFLANYQGGCQ
 285 344
 mGDF-1 ALPETLRGPGGPPALNHAVLRALMHAAAPTGGAGSPQVPERLSPISVLFFDSDNVVLR
 301 359
 hGDF-1 ALPVALSGSGGPPALNHAVLRALMHAAAPGA-ADLPQVPARLSPISVLFFDSDNVVLR
 345 357
 mGDF-1 HYEDMVVDEGGRR
 360 372
 hGDF-1 QYEDMVVDEGGRR

FIG. 13a CONT.

mUOG-1	1	MAAAAAATPRLEAEPMP SYAQMLQRSWASALAAAQCGDCGWLARRGLAEHAHLAAPEL	60
hUOG-1	1	MAAAGPAAAGPTGEEPMPSYAQLVQRGWSALAAARGCTDCGWLARRGLAEHAHLAAPEL	60
mUOG-1	61	LLAVLCA LGWTALRWAAATTHIFRPLAKRCRLQPRDAARLPESAWKLLFYLACWSYCA YLL	120
hUOG-1	61	LLLALGALGWTALRSAAATARLFRPLAKRCCLOPRDAAKMPESAWKFLFYLGWSYSAYLL	120
mUOG-1	121	LGTSYPFFHDPSPSVFYDWRSGMAVPWDIAVAYLLQGSFYCHSIYATVYMDSWRKDSVVML	180
hUOG-1	121	FGTDYPFFHDPSPSVFYDWTGMAVPRDIAAAAYLLQGSFYGHISIYATLYMDTWRKDSVVML	180

FIG. 13b

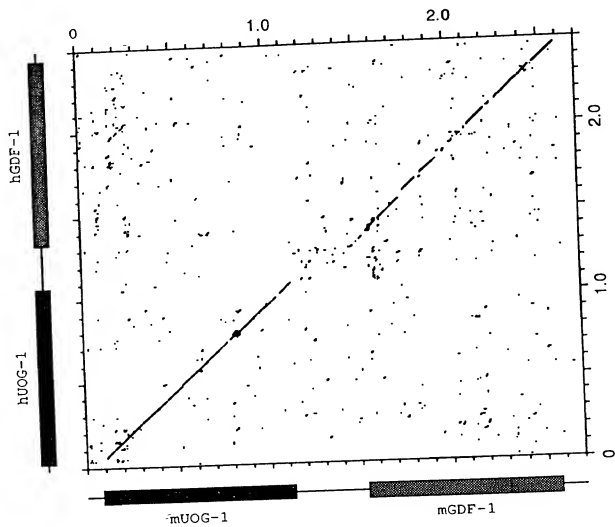


FIG. 13c

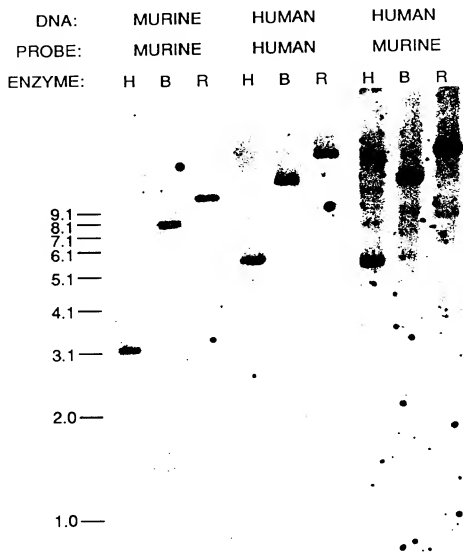


FIG. 14